



Supplementary Figure 4. Portrait of the SNPs across the genomes compared with the standard reference strain *L. monocytogenes* F2365. The mapped SNPs were visualized with the Gingr tool(Ref.1). Compared with F2365, a total of 377 SNPs were observed among the Indian strains. Although an average of 1 SNP per ~8 kb was observed across the genomes, >10 per kb of SNPs were observed near the transposases (marked by the arrow).

1. Treangen TJ, Ondov BD, Koren S, Phillippy AM. The Harvest suite for rapid core-genome alignment and visualization of thousands of intraspecific microbial genomes. *Genome Biol* 2014; 15: 524.